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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/874,991	06/07/2001	James J. Mond	07787.0042	5537

22852 7590 09/08/2004

FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER LLP
1300 I STREET, NW
WASHINGTON, DC 20005

EXAMINER	
MINNIFIELD, NITA M	

ART UNIT	PAPER NUMBER
1645	

DATE MAILED: 09/08/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/874,991	MOND ET AL.	
	Examiner	Art Unit	
	N. M. Minnifield	1645	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *10 June 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-17* is/are pending in the application.

4a) Of the above claim(s) *11-17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-10* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *11-17* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892) 2 sheets

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *10 sheets*. 10/01/01; 9/7/01; 3/11/02

4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .

5) ☐ Notice of Informal Patent Application (PTO-152)

6) ☐ Other: _____.

DETAILED ACTION

1. Applicant's election with traverse of Group I, claims 1-10 and species SEQ ID NO: 2, 5, 6, 7, 12-17, in the reply filed on June 10, 2004 is acknowledged. The traversal is on the ground(s) that for a restriction requirement to be proper, the Examiner must show (1) that the inventions defined by the restricted groups of claims are independent and distinct, and (2) that there would be a serious burden on the Examiner if restriction was not required. M.P.E.P. 803. Applicants assert that the Examiner has focused on only the first part of this two-part test. In order to properly restrict the groups, the Examiner needs to show that there would be a serious burden in examining the claims together. Applicants submit that no such serious burden exists, and respectfully submit that withdrawal of the restriction requirement as to the claims of Groups I, II and V is appropriate. Specifically, because the claims of each group are directed to compositions comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA, this subject matter must be searched for each group. Thus, a thorough search and examination of Groups I, II, and V together does not represent an undue burden and Applicants respectfully request that the Examiner reconsider this restriction requirement. See M.P.E.P. 803 ("If the search and examination of the entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent or distinct inventions." (emphasis added). Applicants expressly reserve their right, under M.P.E.P. 821.04, to add method claims to this application that depend from, or otherwise incorporate all limitations

of, the product claims of Groups I, II, and V for rejoinder with allowed product claims in this application.

This is not found persuasive. With regard to Applicants' assertions that there is no serious search burden to the Examiner to examine Groups I, II and V together, it is noted that a serious search burden is created because the Groups II and V would require additional search for the composition that comprises not only the RNA and DNA as set forth in the invention of Group I, but also the other ingredients claimed in Groups II and V, for example the antigen. The restriction Groups have acquired a separate status in the art as a separate subject for inventive effect and require independent searches. The search for each of the above inventions is not co-extensive particularly with regard to the literature search. A reference, which would anticipate the invention of one group would not necessarily anticipate or make obvious any of the other groups. Moreover, as to the question of burden of search, classification of subject matter is merely one indication of the burdensome nature of the search involved. The literature search, particularly relevant in this art, is not co-extensive and is much more important in evaluating the burden of search. Burden in examining materially different groups having materially different issues also exist. The restriction requirement between Groups I, II and V is maintained.

It is also noted that Applicants expressly reserve their right, under M.P.E.P. 821.04, to add method claims to this application that depend from, or otherwise incorporate all limitations of, the product claims of Group I for rejoinder with allowed product claims in this application. **Process claims that depend from or otherwise include all the limitations of the patentable product** will be entered as a matter of right if the amendment is presented prior to final rejection or allowance, whichever is earlier. Amendments, submitted after final rejection, are

governed by 37 CFR 1.116; amendments submitted after allowance are governed by 37 CFR 1.312.

In the event of rejoinder, the requirement for restriction between the product claims and the rejoined process claims will be withdrawn, and the rejoined process claims will be fully examined for patentability in accordance with 37 CFR 1.104. Thus, to be allowable, the rejoined claims must meet all criteria for patentability including the requirements of 35 U.S.C. 101, 102, 103, and 112. Until an elected product claim is found allowable, an otherwise proper restriction requirement between product claims and process claims may be maintained. Withdrawn process claims that are not commensurate in scope with an allowed product claim will not be rejoined. See "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai, In re Brouwer* and 35 U.S.C. § 103(b)," 1184 O.G. 86 (March 26, 1996). Additionally, in order to retain the right to rejoinder in accordance with the above policy, Applicant is advised that the process claims should be amended during prosecution either to maintain dependency on the product claims or to otherwise include the limitations of the product claims. **Failure to do so may result in a loss of the right to rejoinder.**

Further, note that the prohibition against double patenting rejections of 35 U.S.C. 121 does not apply where the restriction requirement is withdrawn by the examiner before the patent issues. See MPEP § 804.01.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 11-17 have been withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no

allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on June 10, 2004.

3. It is noted that elected SEQ ID NO: 2, 5, 6, and 7 have an effective filing date of June 7, 2000. These sequences were first disclosed in the provisional application 60/209797, filed June 7, 2000. Elected SEQ ID NO: 12-17 have an effective filing date of June 7, 2001. These sequences were first disclosed in the non-provisional application 09/874991, filed June 7, 2001.

4. Claims 8-10 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for *in vitro* use of the immunostimulatory compositions, does not reasonably provide enablement for *in vivo* use of the immunostimulatory compositions. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

The claims are directed to an immunostimulatory composition comprising at least a first oligonucleotide and a second oligonucleotide, wherein both the first and second oligonucleotides each contain at least one RNA region and at least one DNA region, wherein at least one terminus of each oligonucleotide comprises RNA. Claims are also recite that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile. Claims are directed to an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA.

It is noted that the compositions contemplate both *in vitro* and *in vivo* use of these compositions.

The specification discloses *in vitro* methods (simulation of Th1 And Th2 type cytokine production, release of IL-6, release of IFN-gamma, B cell proliferation, stimulation of IgM secretion) using human peripheral lymphocytes and SEQ ID NO: 2, 5, 6, 7, HDR (hybrid DNA and RNA) and SEQ ID NO: 1 (only DNA, as a control) (see specification examples 2-7 on pages 34-47 and Tables 1-9). The specification teaches that the HDR does indeed stimulate different immune stimulation profiles, but only via *in vitro* means. Applicants speculate in the specification that, "it is expected that the HDRs of the invention, including mixtures of HDRs that elicit complementary patterns of activation, will provide correspondingly superior improvement to Thl and Th2 responses in a patient as compared to DNA-based oligonucleotides." (p. 36). However, the specification does set forth any enablement for HDRs eliciting a different immune stimulation profile in an animal or patient or adjuvant activity in an animal or patient. Examples 8-10 (see pages 48-50 of the specification) set forth a prophetic protocol of how one of skill in the art would do these *in vivo* experiments, not that there were actually performed or that the immune stimulation was achieved in the same manner as for the *in vitro* experiments in Examples 2-7. Example 8 states, that "HDR injected mice will show increased levels of total IgM as opposed to the PBS injected controls." (p. 48). Example 9 only shows *in vivo* use of SEQ ID NO: 2. Example 10 states that the "HDR injected animals *will show* elevated levels of anti-BSA ...". (p. 50). The specification further asserts that the list of HDRs (see pages 51-64) are illustrative sequences have been selected in light of ODN sequences known in the art to posses immunostimulatory activity (innate, global,

cellular and/or humoral), and in light of the surprising observation reported herein that hybrid RNA-DNA ONDs (HDRs) possess robust immunostimulatory activity both *in vitro* an *in vivo*. Using the teachings of Examples 1-10, or other assays commonly used in the art, the skilled artisan will recognize that such HDRs, and all other HDR sequences within the scope of the invention can be assayed *in vitro* or *in vivo* for immunostimulatory activity (see p. 51). However, none of the sequences listed on pages 51-64 have been tested and they are not of the same structure as the tested SEQ ID NO: 2. SEQ ID NO: 2 is a RDR (meaning it has RNA at both termini and a DNA, CpG, center) while SEQ ID NO: 12-17 are DR (meaning only one terminus is RNA). It is not clear that a DR will function in the same manner as a RDR in either an *in vitro* or *in vivo* situation.

The state of the art is not clear with regard to the *in vivo* use of a hybrid RNA/DNA. Cong et al 2003 (BBRC, 2003, 310:1133-1139) teach that hybrid DNA/RNA provide similar *in vitro* results as set forth in the specification, but does not teach that this is yet possible *in vivo*. Cong et al indicate that these compounds *may* permit the development of therapeutic agents for use against cancer, asthma, allergy and infectious diseases and as adjuvant, but this has not yet been accomplished (pp.1137-1138). The art only teaches the *in vitro* methods of these hybrid compounds. In view of the lack of teaching and guidance in the specification and the unpredictability in the art with regard to *in vivo* use of these hybrids to elicit a different immune stimulation profile there would be undue experimentation necessary for a skilled artisan to practice the scope of the claimed invention.

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

6. Claims 1-10 are rejected under 35 U.S.C. 102(e) as being anticipated by Raz et al (6534062 6613751 or 6552006).

Raz et al, 6534062 for example, discloses a RNA/DNA hybrid and the DNA has a CpG motif (col. 7, l. 1-33; cols. 20-21). Raz et al discloses modifications of the phosphate backbone, which include a phosphorathioate modification (col. 7). The prior art anticipates the claimed invention.

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA", it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of "adjuvant" is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior

art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and In re Fitzgerald et al., 205 USPQ 594.

7. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Fosnaugh et al 1989 (Molecular and Cellular Biology, Nov. 1989, 9/11:5215-5218).

Fosnaugh et al disclose the elected SEQ ID NO: 7. It is noted that the claims are directed to an immunostimulatory composition comprising: at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA. The prior art discloses the RNA at either or both termini and a DNA sequence that has a CpG motif as claimed.

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising

both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA", it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of "adjuvant" is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and In re Fitzgerald et al., 205 USPQ 594.

8. Claims 1-10 are rejected under 35 U.S.C. 102(e) as being anticipated by Lees et al 6632923 or Dumas et al 6639063.

Lees et al discloses the elected species SEQ ID NO: 16 (see SEQ ID NO: 51 of the patent).

Dumas et al discloses the elected species SEQ ID NO: 7 (see SEQ ID NO: 11708 of the patent).

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA", it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of "adjuvant" is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and In re Fitzgerald et al., 205 USPQ 594.

9. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Accession No. AP000792 and AP000728 published in the Database 1999.

Accession No. AP000792 and AP000728 disclose elected species SEQ ID NO: 6 (see the attached sequence search printout).

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA", it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of "adjuvant" is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and In re Fitzgerald et al., 205 USPQ 594.

10. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Bonaldo et al Genome Research, 1996, 6/9:791-806.

Bonaldo et al discloses the elected species SEQ ID NO: 6 (see the attached sequence search printout).

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA", it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of "adjuvant" is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and In re Fitzgerald et al., 205 USPQ 594.

11. No claims are allowed.

12. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is 571-272-0860. The examiner can normally be reached on M-F (8:00-5:30) Second Friday Off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R.F. Smith can be reached on 571-272-0864. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

N M Minnifield
Primary Examiner
Art Unit 1645

NMM
August 31, 2004

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;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 12427
;   LENGTH: 129
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-12427

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  Best Local Similarity   93.3%;  Pred. No. 13;
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Qy          1 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
              ||||||||||||||::||||||||||||||
Db         97 AAAAAAAAAAAAAAAMSAAAAAAAAAAAAAA 126


RESULT 3
US-09-621-976-11708
; Sequence 11708, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 11708
;   LENGTH: 128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10,110
;   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-11708

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  Best Local Similarity   96.7%;  Pred. No. 14;
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Qy          1 AAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
              ||||||||||||| ||||||||||||||
Db         97 AAAAAAAAAAAAANCGAAAAAAAAAAAAAA 126


RESULT 4
US-09-621-976-17033
; Sequence 17033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 17033
;   LENGTH: 254
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-17033

  Query Match             96.0%;  Score 28.8;  DB 4;  Length 254;
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Qy          1 AAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
              ||||||||||||||:::|||||||||||||
Db        222 AAAAAAAAAAAAARSSAAAAAAAAAAAAAA 251


RESULT 5
US-09-621-976-14176
; Sequence 14176, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 14176
;   LENGTH: 77
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-14176

  Query Match             94.7%;  Score 28.4;  DB 4;  Length 77;
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Qy          1 AAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
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Db         47 AAAAAAAAAAAAAAARGAAAAAAAAAAAAAA 76


RESULT 6
US-09-621-976-13606
; Sequence 13606, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 13606
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-13606

  Query Match             94.7%;  Score 28.4;  DB 4;  Length 183;
  Best Local Similarity   96.7%;  Pred. No. 19;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
              ||||||||||||||| ||||||||||||||
Db        132 AAAAAAAAAAAAAAAGAAAAAAAAAAAAAA 161


RESULT 7
US-09-621-976-10240
; Sequence 10240, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
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FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide~Synthetic DNA/RNA oligonucleotide"
ORIGIN

  Query Match             100.0%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
              ||||||||||||||||||||||||||||||
Db          1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30


RESULT 2
AP000792
LOCUS       AP000792              159712 bp    DNA     linear   HTG 30-MAY-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-792M23 map 11q14, WORKING
            DRAFT SEQUENCE, 20 unordered pieces.
ACCESSION   AP000792
VERSION     AP000792.2  GI:8118948
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 159712)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 159,712 genomic DNA of 11q14
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 159712)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     On May 31, 2000 this sequence version replaced gi:6997629.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft11
                Center clone name: RP11-792M23
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 144304 bases at least Q40
                Consensus quality: 152360 bases at least Q30
                Consensus quality: 156239 bases at least Q20
                Insert size: 157812; sum-of-contigs
                Quality coverage: 4.71x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            20 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
            as soon as it is available and the accession number will be
            preserved
                    1     20543 contig of  20543 bp in length
                20644     41423 contig of  20780 bp in length
                41524     58072 contig of  16549 bp in length
                58173     74856 contig of  16684 bp in length
                74957     90767 contig of  15811 bp in length
                90868    103540 contig of  12673 bp in length
               103641    112882 contig of   9242 bp in length
               112983    118482 contig of   5500 bp in length
               118583    126178 contig of   7596 bp in length
               126279    132359 contig of   6081 bp in length
               132460    137425 contig of   4966 bp in length
               137526    141745 contig of   4220 bp in length
               141846    145942 contig of   4097 bp in length
               146043    148240 contig of   2198 bp in length
               148341    150674 contig of   2334 bp in length
               150775    152334 contig of   1560 bp in length
               152435    154471 contig of   2037 bp in length
               154572    156657 contig of   2086 bp in length
               156758    158548 contig of   1791 bp in length
               158649    159712 contig of   1064 bp in length
            Sequence updated (26-May-2000).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    20543: contig of 20543 bp in length
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            *   20644    41423: contig of 20780 bp in length
            *   41424    41523: gap of 100 bp
            *   41524    58072: contig of 16549 bp in length
            *   58073    58172: gap of 100 bp
            *   58173    74856: contig of 16684 bp in length
            *   74857    74956: gap of 100 bp
            *   74957    90767: contig of 15811 bp in length
            *   90768    90867: gap of 100 bp
            *   90868   103540: contig of 12673 bp in length
            *  103541   103640: gap of 100 bp
            *  103641   112882: contig of 9242 bp in length
            *  112883   112982: gap of 100 bp
            *  112983   118482: contig of 5500 bp in length
            *  118483   118582: gap of 100 bp
            *  118583   126178: contig of 7596 bp in length
            *  126179   126278: gap of 100 bp
            *  126279   132359: contig of 6081 bp in length
            *  132360   132459: gap of 100 bp
            *  132460   137425: contig of 4966 bp in length
            *  137426   137525: gap of 100 bp
            *  137526   141745: contig of 4220 bp in length
            *  141746   141845: gap of 100 bp
            *  141846   145942: contig of 4097 bp in length
            *  145943   146042: gap of 100 bp
            *  146043   148240: contig of 2198 bp in length
            *  148241   148340: gap of 100 bp
            *  148341   150674: contig of 2334 bp in length
            *  150675   150774: gap of 100 bp
            *  150775   152334: contig of 1560 bp in length
            *  152335   152434: gap of 100 bp
            *  152435   154471: contig of 2037 bp in length
            *  154472   154571: gap of 100 bp
            *  154572   156657: contig of 2086 bp in length
            *  156658   156757: gap of 100 bp
            *  156758   158548: contig of 1791 bp in length
            *  158549   158648: gap of 100 bp
            *  158649   159712: contig of 1064 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q14"
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     misc_feature    1. .20543
                     /note="assembly_fragment clone_end:SP6 vector_side:left"
     misc_feature    20644. .41423
                     /note="assembly_fragment"
     misc_feature    41524. .58072
                     /note="assembly_fragment"
     misc_feature    58173. .74856
                     /note="assembly_fragment"
     misc_feature    74957. .90767
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     misc_feature    90868. .103540
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     misc_feature    103641. .112882
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     misc_feature    112983. .118482
                     /note="assembly_fragment clone_end:T7 vector_side:left"
     misc_feature    118583. .126178
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     misc_feature    126279. .132359
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     misc_feature    137526. .141745
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     misc_feature    141846. .145942
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     misc_feature    146043. .148240
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     misc_feature    148341. .150674
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                     /note="assembly_fragment"
ORIGIN

  Query Match             100.0%;  Score 30;  DB 2;  Length 159712;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
              ||||||||||||||||||||||||||||||
Db      20446 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 20475


RESULT 3
AP000728
LOCUS       AP000728              150594 bp    DNA     linear   HTG 30-MAY-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-698G11 map 11q14, WORKING
            DRAFT SEQUENCE, 48 unordered pieces.
ACCESSION   AP000728
VERSION     AP000728.2  GI:8118897
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 150594)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 150,594 genomic DNA of 11q14
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 150594)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     On May 31, 2000 this sequence version replaced gi:6997583.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft11
                Center clone name: RP11-698G11
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 126690 bases at least Q40
                Consensus quality: 137135 bases at least Q30
                Consensus quality: 143169 bases at least Q20
                Insert size: 145894; sum-of-contigs
                Quality coverage: 4.08x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            48 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
            as soon as it is available and the accession number will be
            preserved
                  1     7885 contig of   7885 bp in length
               7986    16310 contig of   8325 bp in length
              16411    22088 contig of   5678 bp in length
              22189    28358 contig of   6170 bp in length
              28459    34160 contig of   5702 bp in length
              34261    39101 contig of   4841 bp in length
              39202    44288 contig of   5087 bp in length
              44389    50127 contig of   5739 bp in length
              50228    55556 contig of   5329 bp in length
              55657    58778 contig of   3122 bp in length
              58879    62612 contig of   3734 bp in length
              62713    66184 contig of   3472 bp in length
              66285    70737 contig of   4453 bp in length
              70838    75172 contig of   4335 bp in length
              75273    79642 contig of   4370 bp in length
              79743    83579 contig of   3837 bp in length
              83680    86336 contig of   2657 bp in length
              86437    89885 contig of   3449 bp in length
              89986    93305 contig of   3320 bp in length
              93406    96389 contig of   2984 bp in length
              96490    99699 contig of   3210 bp in length
              99800   102152 contig of   2353 bp in length
             102253   105419 contig of   3167 bp in length
             105520   108048 contig of   2529 bp in length
             108149   110751 contig of   2603 bp in length
             110852   114363 contig of   3512 bp in length
             114464   115521 contig of   1058 bp in length
             115622   117656 contig of   2035 bp in length
             117757   119830 contig of   2074 bp in length
             119931   122309 contig of   2379 bp in length
             122410   124103 contig of   1694 bp in length
             124204   126256 contig of   2053 bp in length
             126357   128377 contig of   2021 bp in length
             128478   130309 contig of   1832 bp in length
             130410   131990 contig of   1581 bp in length
             132091   133536 contig of   1446 bp in length
             133637   135395 contig of   1759 bp in length
             135496   137087 contig of   1592 bp in length
             137188   138305 contig of   1118 bp in length
             138406   139438 contig of   1033 bp in length
             139539   141650 contig of   2112 bp in length
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    141751    143058 contig of   1308 bp in length
    143159    144610 contig of   1452 bp in length
    144711    145763 contig of   1053 bp in length
    145864    146911 contig of   1048 bp in length
    147012    148183 contig of   1172 bp in length
    148284    149304 contig of   1021 bp in length
    149405    150594 contig of   1190 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*         1      7885: contig of 7885 bp in length
*      7886      7985: gap of 100 bp
*      7986     16310: contig of 8325 bp in length
*     16311     16410: gap of 100 bp
*     16411     22088: contig of 5678 bp in length
*     22089     22188: gap of 100 bp
*     22189     28358: contig of 6170 bp in length
*     28359     28458: gap of 100 bp
*     28459     34160: contig of 5702 bp in length
*     34161     34260: gap of 100 bp
*     34261     39101: contig of 4841 bp in length
*     39102     39201: gap of 100 bp
*     39202     44288: contig of 5087 bp in length
*     44289     44388: gap of 100 bp
*     44389     50127: contig of 5739 bp in length
*     50128     50227: gap of 100 bp
*     50228     55556: contig of 5329 bp in length
*     55557     55656: gap of 100 bp
*     55657     58778: contig of 3122 bp in length
*     58779     58878: gap of 100 bp
*     58879     62612: contig of 3734 bp in length
*     62613     62712: gap of 100 bp
*     62713     66184: contig of 3472 bp in length
*     66185     66284: gap of 100 bp
*     66285     70737: contig of 4453 bp in length
*     70738     70837: gap of 100 bp
*     70838     75172: contig of 4335 bp in length
*     75173     75272: gap of 100 bp
*     75273     79642: contig of 4370 bp in length
*     79643     79742: gap of 100 bp
*     79743     83579: contig of 3837 bp in length
*     83580     83679: gap of 100 bp
*     83680     86336: contig of 2657 bp in length
*     86337     86436: gap of 100 bp
*     86437     89885: contig of 3449 bp in length
*     89886     89985: gap of 100 bp
*     89986     93305: contig of 3320 bp in length
*     93306     93405: gap of 100 bp
*     93406     96389: contig of 2984 bp in length
*     96390     96489: gap of 100 bp
*     96490     99699: contig of 3210 bp in length
*     99700     99799: gap of 100 bp
*     99800    102152: contig of 2353 bp in length
*    102153    102252: gap of 100 bp
*    102253    105419: contig of 3167 bp in length
*    105420    105519: gap of 100 bp
*    105520    108048: contig of 2529 bp in length
*    108049    108148: gap of 100 bp
*    108149    110751: contig of 2603 bp in length
*    110752    110851: gap of 100 bp
*    110852    114363: contig of 3512 bp in length
*    114364    114463: gap of 100 bp
*    114464    115521: contig of 1058 bp in length
*    115522    115621: gap of 100 bp
*    115622    117656: contig of 2035 bp in length
*    117657    117756: gap of 100 bp
*    117757    119830: contig of 2074 bp in length
*    119831    119930: gap of 100 bp
*    119931    122309: contig of 2379 bp in length
*    122310    122409: gap of 100 bp
*    122410    124103: contig of 1694 bp in length
*    124104    124203: gap of 100 bp
*    124204    126256: contig of 2053 bp in length
*    126257    126356: gap of 100 bp
*    126357    128377: contig of 2021 bp in length
*    128378    128477: gap of 100 bp
*    128478    130309: contig of 1832 bp in length
*    130310    130409: gap of 100 bp
*    130410    131990: contig of 1581 bp in length
*    131991    132090: gap of 100 bp
*    132091    133536: contig of 1446 bp in length
*    133537    133636: gap of 100 bp
*    133637    135395: contig of 1759 bp in length
*    135396    135495: gap of 100 bp
*    135496    137087: contig of 1592 bp in length
*    137088    137187: gap of 100 bp
*    137188    138305: contig of 1118 bp in length
*    138306    138405: gap of 100 bp
*    138406    139438: contig of 1033 bp in length
*    139439    139538: gap of 100 bp
*    139539    141650: contig of 2112 bp in length
*    141651    141750: gap of 100 bp
*    141751    143058: contig of 1308 bp in length
*    143059    143158: gap of 100 bp
*    143159    144610: contig of 1452 bp in length
*    144611    144710: gap of 100 bp
*    144711    145763: contig of 1053 bp in length
*    145764    145863: gap of 100 bp
*    145864    146911: contig of 1048 bp in length
*    146912    147011: gap of 100 bp
*    147012    148183: contig of 1172 bp in length
*    148184    148283: gap of 100 bp

  Query Match             96.7%;  Score 29;  DB 2;  Length 150594;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAAAAAAAAAACCCGGGAAAAAAAAAAA 29
              |||||||||||||||||||||||||||||
Db     110717 AAAAAAAAAAAAACCCGGGAAAAAAAAAAA 110745


RESULT 4
AB127405
LOCUS       AB127405               4127 bp    mRNA    linear   PRI 04-DEC-2003
DEFINITION  Homo sapiens SNIP mRNA for SNAP-25-interacting protein, complete
            cds.
ACCESSION   AB127405
VERSION     AB127405.1  GI:38678111
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sugiyama,A., Inoue,H. and Oka,M.
  TITLE     Homo sapiens cDNA, SNIP homolog
  JOURNAL   Published Only in Database (2003)
REFERENCE   2  (bases 1 to 4127)
  AUTHORS   Sugiyama,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-DEC-2003) Akio Sugiyama, TOYOBO CO.,LTD; Toyocyo
            10-24, Tsuruga, Fukui 914-0047, Japan
            (E-mail:akio_sugiyama@bio.toyobo.co.jp, Tel:81-770-22-7643,
            Fax:80-770-22-7671)
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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Please mail my Action

Fax:81-75-705-1113)
COMMENT Ciona intestinalis cDNA Project (URL:
http://ghost.zool.kyoto-u.ac.jp/indexr1.html).
FEATURES Location/Qualifiers
source 1. .1458
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg056p11"
ORIGIN

Query Match 100.0%; Score 30; DB 3; Length 1458;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
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RESULT 6
AY080787
LOCUS AY080787 1538 bp mRNA linear PLN 18-SEP-2002
DEFINITION Arabidopsis thaliana putative enoyl-CoA hydratase (At4g31810) mRNA, complete cds.
ACCESSION AY080787
VERSION AY080787.1 GI:19424018
KEYWORDS PLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1538)
AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE Arabidopsis Full Length cDNA Clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1538)
AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
FEATURES Location/Qualifiers
source 1. .1538
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="RAFL05-21-G10 (R10305)"
/ecotype="Columbia"
/note="This clone is in a modified pBluescript vector (Lambda ZAP) as a XhoI/SstI insert."
gene 1. .1538
/gene="At4g31810"
5'UTR 1. .19
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CDS 20. .1249
/gene="At4g31810"
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/protein_id="AAL87270.1"
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DVLSLYHSINEGNTEESKLPFENLYKFVYLQGTYLKPNIAIMDGVTMGCGGGISLPGM
FRVATDKTVLAHPEVQIGFHPDAGASYYLSRLPGYLGEYLALTGQKLNGVEMIACGLA
THYCLNARLPLIEERIGKLLTDDPAVIEDSLAQYGDLVYPDSSSVLHKIELIDKYFGL
DTVEEIIEAMENEAANSCNEWCKKTLKQIKEASPLSLKITLQSIREGRFQTLDQCLTH
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3'UTR 1250. .1538
/gene="At4g31810"
misc_feature 1521. .1522
/gene="At4g31810"
/note="artifact within poly A tail"
ORIGIN

Query Match 100.0%; Score 30; DB 8; Length 1538;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
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Db 1507 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 1536

RESULT 7
DDISP60A
LOCUS DDISP60A 1625 bp DNA linear INV 18-MAY-1994
DEFINITION D.discoideum spore coat protein SP60 gene, complete cds.
ACCESSION M26239
VERSION M26239.1 GI:167885
KEYWORDS major spore coat protein; spore protein.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Fosnaugh,K.L. and Loomis,W.F.
TITLE Spore coat genes SP60 and SP70 of Dictyostelium discoideum
JOURNAL Mol. Cell. Biol. 9 (11), 5215-5218 (1989)
MEDLINE 90097939
PUBMED 2601718
REFERENCE 2 (bases 1 to 1625)
AUTHORS Fosnaugh,K.L.
JOURNAL Unpublished (1990)
COMMENT Original source text: D.discoideum (strain Ax4), DNA (bp 1 to 693), clones pSP[60,60.1], and cDNA to mRNA (bp 694 to 1560), clone SP1.8.
[2] revises [1].
Draft entry and computer readable sequence for [1] kindly submitted by K.Fosnaugh, 13-JUL-1989.

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                     /mol_type="genomic DNA"
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                     /gene="SP60"
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     gene            join(109. .262,384. .1504)
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                     NYHCICGDKIDGVKCVPDCKKARCDDVECPDFHRCVERRGGILSCEFDPPRQPRSLDW
                     AENENDDRDYDDRDYDDDEYDGDYDGRDGDYDGDYDGDYDDDNYYGDDDYDNDWDNDN
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     mat_peptide     join(178. .262,384. .1501)
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                     /product="spore coat protein"
     intron          263. .383
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     exon            384. .1560
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                     /number=2
ORIGIN
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         80 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 109
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RESULT 8
AB047834
LOCUS       AB047834               1683 bp    mRNA    linear   PRI 11-OCT-2001
DEFINITION  Macaca fascicularis brain cDNA, clone:QccE-16296.
ACCESSION   AB047834
VERSION     AB047834.1  GI:9967116
KEYWORDS    fis (full insert sequence).
SOURCE      Macaca fascicularis (crab-eating macaque)
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1
  AUTHORS   Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M.,
            Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
  TITLE     Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
            chromosomes
  JOURNAL   Gene 275 (1), 31-37 (2001)
  MEDLINE   21458551
   PUBMED   11574149
REFERENCE   2  (bases 1 to 1683)
  AUTHORS   Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-2000) Katsuyuki Hashimoto, National Institute of
            Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
            1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
            Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT     Lab host:    TOP10
            Vector:      pME18S-FL3 (Acc.No. AB009864)
            R.  Site1:   DraIII (CACTGTGTG)
            R.  Site2:   DraIII (CACCATGTG)
            Description: 1st strand cDNA was primed with an oligo(dT) primer
            [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
            using specific 5' and 3' primers and amplified by PCR.  The PCR
            product was digested with SfiI and size selection was performed to
            exclude fragments <1.5kb.The SfiI-digested PCR product was cloned
            into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
            the DraIII sites can be used to isolate the cDNA insert.  Libraries
            were constructed by Sugano et al.(University of Tokyo, Institute of
            Medical Science). Custom primer used for sequencing
            ( 5' end primer [CTTCTGCTCTAAAAGCTGCG];
            3' end primer [CGACCTGCAGCTCGAGCACA] ).
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9541"
                     /clone="QccE-16296"
                     /sex="male"
                     /tissue_type="cerebellum cortex"
                     /clone_lib="macaque brain cDNA library QccE"
                     /dev_stage="adult"
                     /lab_host="TOP10"
     CDS             14. .1360
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="BAB12260.1"
                     /db_xref="GI:9967117"
                     /translation="MSGMYRCQTSQYNGFNVKPREALVQLIVQYPPAVEPAFLEIRQG
                     QDRSVTMSCRVLRAYPIRVLTYEWRLGNKLLRTGQFDSQEYTEYPVKSLSNENYGVYN
                     CSIINEAGAGRCSFLVTGKAYAPEFYYDTYNPVWQNRHRVYSYSLQWTQMNPDAVDRI
                     VAYRLGIRQAGQQRWWEQEIKINGNIQKGELITYNLTELIKPEAYEVRLTPLTKFGEG
                     DSTIRVIKYSAPVNPHLREFHCGFEDGNICLFTQDDTDNFDWTKQSTATRNTKYTPNT
                     GPNADRSGSKEGFYMYIETSRPRLEGEKARLLSPVFSIAPKNPYGPTNTAYCPSFFYH
                     MYGQHIGVLNVYLRLKGQTTIENPLWSSSGNKGQRWNEAHVNIYPITSFQLIFEGIRG
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ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 30
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Db       1652 AAAAAAAAAAAAAAACGAAAAAAAAAAAAAA 1681
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RESULT 9
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LOCUS       BT003906               1689 bp    mRNA    linear   PLN 14-FEB-2003
DEFINITION  Arabidopsis thaliana clone RAFL15-13-B15 (R20655) unknown protein
            (At1g72110) mRNA, complete cds.
ACCESSION   BT003906
VERSION     BT003906.1  GI:28393038
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1689)
  AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
            Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C.,
            Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
            Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
            Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
            Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
            Ecker,J.R. and Theologis,A.
  TITLE     Arabidopsis Full Length cDNA Clones
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 27, 2004, 05:18:34 ; Search time 1517.85 Seconds
(without alignments)
590.218 Million cell updates/sec

Title: US-09-874-991C-6
Perfect score: 30
Sequence: 1 aaaaaaaaaaaacccgggaaaaaaaaaaaa 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	100.0	467	10	BE992043	BE992043 UI-M-BZ1-
	2	30	100.0	887	13	BU944962	BU944962 AGENCOURT
	3	29.2	97.3	582	9	AL514409	AL514409 AL514409
	4	29	96.7	244	14	CD215240	CD215240 pgm2n.pk0
	5	29	96.7	333	9	AI837622	AI837622 UI-M-AK0-
	6	29	96.7	427	14	CB476773	CB476773 jns124_H1
	7	28.8	96.0	379	13	BX424970	BX424970 BX424970
	8	28.8	96.0	855	13	BX393666	BX393666 BX393666
	9	28.8	96.0	1201	13	BX393528	BX393528 BX393528
	10	28.8	96.0	1201	13	BX445790	BX445790 BX445790
c	11	28.4	94.7	65	13	BQ389828	BQ389828 NISC_mq09
	12	28.4	94.7	189	13	BU960192	BU960192 AGENCOURT
	13	28.4	94.7	191	9	AI012754	AI012754 EST207205
	14	28.4	94.7	214	9	AU038058	AU038058 AU038058
c	15	28.4	94.7	237	9	AI850987	AI850987 UI-M-BH0-
c	16	28.4	94.7	263	14	CF337553	CF337553 JMT--08-A
	17	28.4	94.7	281	14	CA738092	CA738092 wpi2s.pk0
	18	28.4	94.7	326	10	BE104228	BE104228 UI-R-BX0-
	19	28.4	94.7	369	14	CB721366	CB721366 jnn606C08
	20	28.4	94.7	391	9	AJ541315	AJ541315 AJ541315
	21	28.4	94.7	391	9	AV646715	AV646715 AV646715
	22	28.4	94.7	400	14	CB077538	CB077538 hj56a07.g
	23	28.4	94.7	405	14	CF656383	CF656383 tac53g01.
	24	28.4	94.7	414	13	BQ845683	BQ845683 QGA17G03.
	25	28.4	94.7	421	29	CE230334	CE230334 tigr-gss-
	26	28.4	94.7	442	13	BQ521746	BQ521746 NISC_nl12
	27	28.4	94.7	446	14	CF879286	CF879286 tric019xp
	28	28.4	94.7	473	14	CB079242	CB079242 hp68e08.b
	29	28.4	94.7	478	12	BM117544	BM117544 L0853A12-
	30	28.4	94.7	508	13	BQ527846	BQ527846 NISC_no24
	31	28.4	94.7	513	29	AL952398	AL952398 Arabidops
	32	28.4	94.7	525	12	BI491724	BI491724 df14c02.w
c	33	28.4	94.7	557	13	BQ397970	BQ397970 NISC_mo03
	34	28.4	94.7	644	14	CB346417	CB346417 CAB2SG000
	35	28.4	94.7	672	14	CB319854	CB319854 AGENCOURT
	36	28.4	94.7	696	29	CG789315	CG789315 ZMMBBb026
	37	28.4	94.7	703	13	BU181322	BU181322 AGENCOURT
	38	28.4	94.7	723	9	AV710036	AV710036 AV710036
	39	28.4	94.7	796	14	CD538077	CD538077 kue000107
	40	28.4	94.7	856	28	AZ175573	AZ175573 SP_0132_A
	41	28.4	94.7	877	13	BU531207	BU531207 AGENCOURT
	42	28.4	94.7	886	13	BQ441825	BQ441825 AGENCOURT
	43	28.4	94.7	959	13	BX371183	BX371183 BX371183
c	44	28.4	94.7	1019	14	CF587086	CF587086 AGENCOURT
	45	28.4	94.7	1201	9	AL554915	AL554915 AL554915

ALIGNMENTS

RESULT 1
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LOCUS BE992043 467 bp mRNA linear EST 05-OCT-2000
DEFINITION UI-M-BZ1-bec-d-04-0-UI.s1 NIH_BMAP_MHI2_S1 Mus musculus cDNA clone UI-M-BZ1-bec-d-04-0-UI 3', mRNA sequence.
ACCESSION BE992043
VERSION BE992043.1 GI:10672511
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 467)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the hippocampus tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 1-55, >POLY_A#Simple_repeat 143-277, >POLY_A#Simple_repeat 361-432, >GC_rich#Low_complexity
Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BZ1-bec-d-04-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_MHI2_S1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MHI2_S1 library is a subtracted library derived from NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_TISSUE=hippocampus
TAG_LIB=NIH_BMAP_MHI2_S1
TAG_SEQ=TAGTC"

ORIGIN

Query Match 100.0%; Score 30; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
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Db 207 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 236

RESULT 2
BU944962
LOCUS BU944962 887 bp mRNA linear EST 18-OCT-2002
DEFINITION AGENCOURT_10546565 NIH_MGC_141 Homo sapiens cDNA clone IMAGE:6733176 5', mRNA sequence.
ACCESSION BU944962
VERSION BU944962.1 GI:24133781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3062 row: f column: 23
High quality sequence stop: 303.

FEATURES Location/Qualifiers
source 1. .887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6733176"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_141"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH_MGC_142). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 30; DB 13; Length 887;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
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Db 341 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 370

RESULT 3
AL514409
LOCUS AL514409 582 bp mRNA linear EST 08-MAY-2003
DEFINITION AL514409 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CL0BB009ZC11 3-PRIME, mRNA sequence.
ACCESSION AL514409
VERSION AL514409.2 GI:30464294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12777903.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10492.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB009ZC11FP1&cluster=10492.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BB009ZC11FP1.

FEATURES Location/Qualifiers
source 1. .582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB009ZC11"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"

/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 97.3%; Score 29.2; DB 9; Length 582;
Best Local Similarity 93.3%; Pred. No. 7.1e+03;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
              ||||||||||||||::||||||||||||||
Db        190 AAAAAAAAAAAACCCSSGAAAAAAAAAAAA 219
```

RESULT 4
CD215240
LOCUS CD215240 244 bp mRNA linear EST 20-MAY-2003
DEFINITION pgm2n.pk014.f18 Normalized chicken muscle cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk014.f18 5' similar to no significant hits (pLog(P) > 4), mRNA sequence.
ACCESSION CD215240
VERSION CD215240.1 GI:30955051
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 244)
AUTHORS Cogburn,L.A. and Monsonego-Ornan,E.
TITLE Chicken ESTs from muscle
JOURNAL Unpublished (2002)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES Location/Qualifiers
source 1. .244
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler chickens, Ottawa Research Ctr Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk014.f18"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
/dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. Coli EMDH10B"
/clone_lib="Normalized chicken muscle cDNA library (pgm2n)"
/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

ORIGIN

Query Match 96.7%; Score 29; DB 14; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AAAAAAAAAAAACCCGGGAAAAAAAAAAAA 29
              |||||||||||||||||||||||||||||
Db         52 AAAAAAAAAAAACCCGGGAAAAAAAAAAA 80
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RESULT 5

AI837622
LOCUS AI837622 333 bp mRNA linear EST 14-JUL-1999
DEFINITION UI-M-AK0-adg-d-10-0-UI.s1 NIH_BMAP_MHY Mus musculus cDNA clone UI-M-AK0-adg-d-10-0-UI 3', mRNA sequence.
ACCESSION AI837622
VERSION AI837622.1 GI:5471835
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 333)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .333
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-AK0-adg-d-10-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_MHY"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MHY library is a non-normalized library constructed from mouse hypothalamus. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories.
TAG_TISSUE=hypothalamus
TAG_LIB=NIH_BMAP_MHY
TAG_SEQ=CGGTA"

ORIGIN

Query Match 96.7%; Score 29; DB 9; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
              ||||||||||||||||||||||||||||||
Db        262 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 290
```

RESULT 6
CB476773
LOCUS CB476773 427 bp mRNA linear EST 26-MAR-2003